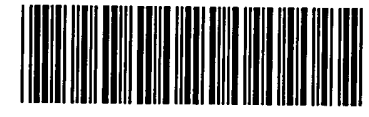


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RAW SEQUENCE LISTING

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3 <110> APPLICANT: PELLETTIER, JERRY
4     GROS, PHILIPPE
5     DUBOW, MICHAEL
7 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS INVOLVING AN ESSENTIAL
8     STAPHYLOCOCCUS AUREUS GENE AND ITS ENCODED PROTEIN
9     STAAU_R9
11 <130> FILE REFERENCE: 073406-0701
13 <140> CURRENT APPLICATION NUMBER: 10/025,222A
14 <141> CURRENT FILING DATE: 2001-12-19
16 <150> PRIOR APPLICATION NUMBER: 60/256,349
17 <151> PRIOR FILING DATE: 2000-12-19
19 <160> NUMBER OF SEQ ID NOS: 41
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1800
25 <212> TYPE: DNA
26 <213> ORGANISM: Staphylococcus aureus
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30 gtaagtgaat atgtaaaatt agaaaagaga ggacgcaatt atagaggttt gtgtcctttt 120
31 catgatgaaa agacaccttc atttacagtt tctgaagata aacaaatttg tcattgtttt 180
32 ggttgtaaaa aaggtggcaa tgtttttcaa ttactcaag aaattaaaga catatcattt 240
33 gttgaagcgg ttaaagaatt aggtgataga gttaatgttg ctgtagatat tgaggcaaca 300
34 caatctaact caaatgttca aattgcttct gatgatttac aaatgattga aatgcatgag 360
35 ttaatacaag aattttatta ttacgcttta acaaagacag tcgaaggcga acaagcatta 420
36 acgtacttac aagaacgtgg ttttacagat gcgcttatta aagagcgagg cattggcttt 480
37 gcacccgata gtcacattt ttgtcatgat tttcttcaaa aaaagggtta cgatattgaa 540
38 ttagcatatg aagccggatt attatcacgt aacgaagaaa atttcagtta ttacgataga 600
39 tttcgaaatc gtattatgtt tcctttgaaa aatgcgcaag gaagaattgt tggatattca 660
40 ggtcgaacat ataccggtca agaaccaaaa tacttaaata gtctgaaac acctatcttt 720
41 caaaaaagaa agttgttata caacttagat aaagcgcgta aatcaattag aaaattagat 780
42 gaaatcgtat tactagaagg ttttatggat gttataaaat ctgatactgc tggcttgaaa 840
43 aacgttggtg caacaatggg tacacagttg tcagatgaac atattacttt tatacgaaag 900
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45 aaaacaggtc aaaattttgtt acagcaaggg ctaaattgtat ttgttatata attgccatca 1020
46 ggcattggtc cggatgaata cattggtaag tatggcaacg atgcatttac tgcttttgta 1080
47 aaaaatgaca aaaagtcatt tgcacattat aaagtgaagta tattaagaaga tgaaattgca 1140
48 cataatgacc tttcatatga acgttatgtt aaagaactaa gtcatgatat ttcgcttatg 1200
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51 gatgagtatg gcggttacat tgaacctgag ccaattggta tggcacaatt tgacaatttg 1380
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54 gtattcgaag tcttacatga tttttatgcg gaaaatgac aatataatat cagtgatgct 1560  
 55 gtgcagtatg ttaattcaaa tgagttgaga gaaacactaa ttagcttaga acaatataat 1620  
 56 ttgaatgacg aaccatatga aaatgaaatt gatgattatg tcaatgttat taatgaaaaa 1680  
 57 ggacaagaaa caattgagtc attgaatcat aaattaaggg aagctacaag gattggcgat 1740  
 58 gtagaattac aaaaatacta tttacagcaa attgttgcta agaataaaga acgcatgtag 1800

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62 &lt;211&gt; LENGTH: 599

63 &lt;212&gt; TYPE: PRT

64 &lt;213&gt; ORGANISM: Staphylococcus aureus

66 &lt;400&gt; SEQUENCE: 2

67 Leu Arg Ile Asp Gln Ser Ile Ile Asn Glu Ile Lys Asp Lys Thr Asp  
 68 1 5 10 15  
 70 Ile Leu Asp Leu Val Ser Glu Tyr Val Lys Leu Glu Lys Arg Gly Arg  
 71 20 25 30  
 73 Asn Tyr Ile Gly Leu Cys Pro Phe His Asp Glu Lys Thr Pro Ser Phe  
 74 35 40 45  
 76 Thr Val Ser Glu Asp Lys Gln Ile Cys His Cys Phe Gly Cys Lys Lys  
 77 50 55 60  
 79 Gly Gly Asn Val Phe Gln Phe Thr Gln Glu Ile Lys Asp Ile Ser Phe  
 80 65 70 75 80  
 82 Val Glu Ala Val Lys Glu Leu Gly Asp Arg Val Asn Val Ala Val Asp  
 83 85 90 95  
 85 Ile Glu Ala Thr Gln Ser Asn Ser Asn Val Gln Ile Ala Ser Asp Asp  
 86 100 105 110  
 88 Leu Gln Met Ile Glu Met His Glu Leu Ile Gln Glu Phe Tyr Tyr Tyr  
 89 115 120 125  
 91 Ala Leu Thr Lys Thr Val Glu Gly Glu Gln Ala Leu Thr Tyr Leu Gln  
 92 130 135 140  
 94 Glu Arg Gly Phe Thr Asp Ala Leu Ile Lys Glu Arg Gly Ile Gly Phe  
 95 145 150 155 160  
 97 Ala Pro Asp Ser Ser His Phe Cys His Asp Phe Leu Gln Lys Lys Gly  
 98 165 170 175  
 100 Tyr Asp Ile Glu Leu Ala Tyr Glu Ala Gly Leu Leu Ser Arg Asn Glu  
 101 180 185 190  
 103 Glu Asn Phe Ser Tyr Tyr Asp Arg Phe Arg Asn Arg Ile Met Phe Pro  
 104 195 200 205  
 106 Leu Lys Asn Ala Gln Gly Arg Ile Val Gly Tyr Ser Gly Arg Thr Tyr  
 107 210 215 220  
 109 Thr Gly Gln Glu Pro Lys Tyr Leu Asn Ser Pro Glu Thr Pro Ile Phe  
 110 225 230 235 240  
 112 Gln Lys Arg Lys Leu Leu Tyr Asn Leu Asp Lys Ala Arg Lys Ser Ile  
 113 245 250 255  
 115 Arg Lys Leu Asp Glu Ile Val Leu Leu Glu Gly Phe Met Asp Val Ile  
 116 260 265 270  
 118 Lys Ser Asp Thr Ala Gly Leu Lys Asn Val Val Ala Thr Met Gly Thr  
 119 275 280 285  
 121 Gln Leu Ser Asp Glu His Ile Thr Phe Ile Arg Lys Leu Thr Ser Asn  
 122 290 295 300  
 124 Ile Thr Leu Met Phe Asp Gly Asp Phe Ala Gly Ser Glu Ala Thr Leu

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125 305          310          315          320
127 Lys Thr Gly Gln Asn Leu Leu Gln Gln Gly Leu Asn Val Phe Val Ile
128          325          330          335
130 Gln Leu Pro Ser Gly Met Asp Pro Asp Glu Tyr Ile Gly Lys Tyr Gly
131          340          345          350
133 Asn Asp Ala Phe Thr Ala Phe Val Lys Asn Asp Lys Lys Ser Phe Ala
134          355          360          365
136 His Tyr Lys Val Ser Ile Leu Lys Asp Glu Ile Ala His Asn Asp Leu
137          370          375          380
139 Ser Tyr Glu Arg Tyr Leu Lys Glu Leu Ser His Asp Ile Ser Leu Met
140 385          390          395          400
142 Lys Ser Ser Ile Leu Gln Gln Lys Ala Leu Asn Asp Val Ala Pro Phe
143          405          410          415
145 Phe Asn Val Ser Pro Glu Gln Leu Ala Asn Glu Ile Gln Phe Asn Gln
146          420          425          430
148 Ala Pro Ala Asn Tyr Tyr Pro Glu Asp Glu Tyr Gly Gly Tyr Ile Glu
149          435          440          445
151 Pro Glu Pro Ile Gly Met Ala Gln Phe Asp Asn Leu Ser Arg Gln Glu
152          450          455          460
154 Lys Ala Glu Arg Ala Phe Leu Lys His Leu Met Arg Asp Lys Asp Thr
155 465          470          475          480
157 Phe Leu Asn Tyr Tyr Glu Ser Val Asp Lys Asp Asn Phe Thr Asn Gln
158          485          490          495
160 His Phe Lys Tyr Val Phe Glu Val Leu His Asp Phe Tyr Ala Glu Asn
161          500          505          510
163 Asp Gln Tyr Asn Ile Ser Asp Ala Val Gln Tyr Val Asn Ser Asn Glu
164          515          520          525
166 Leu Arg Glu Thr Leu Ile Ser Leu Glu Gln Tyr Asn Leu Asn Asp Glu
167          530          535          540
169 Pro Tyr Glu Asn Glu Ile Asp Asp Tyr Val Asn Val Ile Asn Glu Lys
170 545          550          555          560
172 Gly Gln Glu Thr Ile Glu Ser Leu Asn His Lys Leu Arg Glu Ala Thr
173          565          570          575
175 Arg Ile Gly Asp Val Glu Leu Gln Lys Tyr Tyr Leu Gln Gln Ile Val
176          580          585          590
178 Ala Lys Asn Lys Glu Arg Met
179          595
182 <210> SEQ ID NO: 3
183 <211> LENGTH: 216
184 <212> TYPE: DNA
185 <213> ORGANISM: Staphylococcus aureus
187 <400> SEQUENCE: 3
188 atgaatataa tgcaattcaa aagcttattg aaatcgatgt atgaagagac aaagcaaagc 60
189 gacccgattg tagcaaatgt atatatcgag actggttggg cgggtcaatag attgttgga 120
190 aataacgagt tatcgctttt cgatgattac gacagagttg aaaagaaaat catgaatgaa 180
191 atcaactgga agaaaacaca cattaaggag tggttaa 216
194 <210> SEQ ID NO: 4
195 <211> LENGTH: 71
196 <212> TYPE: PRT

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197 <213> ORGANISM: Staphylococcus aureus
199 <400> SEQUENCE: 4
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201   1           5           10           15
203 Thr Lys Gln Ser Asp Pro Ile Val Ala Asn Val Tyr Ile Glu Thr Gly
204           20           25           30
206 Trp Ala Val Asn Arg Leu Leu Asp Asn Asn Glu Leu Ser Pro Phe Asp
207           35           40           45
209 Asp Tyr Asp Arg Val Glu Lys Lys Ile Met Asn Glu Ile Asn Trp Lys
210           50           55           60
212 Lys Thr His Ile Lys Glu Cys
213   65           70
216 <210> SEQ ID NO: 5
217 <211> LENGTH: 120
218 <212> TYPE: DNA
219 <213> ORGANISM: Staphylococcus aureus
221 <400> SEQUENCE: 5
222 ggacaagaaa caattgagtc attgaatcat aaattaaggg aagctacaag gattggcgat 60
223 gtagaattac aaaaatacta ttacagcaa attgttgcta agaataaaga acgcatgtag 120
226 <210> SEQ ID NO: 6
227 <211> LENGTH: 39
228 <212> TYPE: PRT
229 <213> ORGANISM: Staphylococcus aureus
231 <400> SEQUENCE: 6
232 Gly Gln Glu Thr Ile Glu Ser Leu Asn His Lys Leu Arg Glu Ala Thr
233   1           5           10           15
235 Arg Ile Gly Asp Val Glu Leu Gln Lys Tyr Tyr Leu Gln Gln Ile Val
236           20           25           30
238 Ala Lys Asn Lys Glu Arg Met
239           35
242 <210> SEQ ID NO: 7
243 <211> LENGTH: 34
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
250 <400> SEQUENCE: 7
251 cgcggatccc tatccttttt cattaataac attg 34
254 <210> SEQ ID NO: 8
255 <211> LENGTH: 27
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
262 <400> SEQUENCE: 8
263 ccggaattct tgcgaataga tcaatcg 27
266 <210> SEQ ID NO: 9
267 <211> LENGTH: 28
268 <212> TYPE: DNA

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269 <213> ORGANISM: Artificial Sequence
271 <220> FEATURE:
272 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
274 <400> SEQUENCE: 9
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278 <210> SEQ ID NO: 10
279 <211> LENGTH: 27
280 <212> TYPE: DNA
281 <213> ORGANISM: Artificial Sequence
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
286 <400> SEQUENCE: 10
287 ccggaattca tgatagggtt gtgtcct                27
290 <210> SEQ ID NO: 11
291 <211> LENGTH: 29
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial Sequence
295 <220> FEATURE:
296 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
298 <400> SEQUENCE: 11
299 ccggaattcc caaaatacct aaatagtcc                29
302 <210> SEQ ID NO: 12
303 <211> LENGTH: 27
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
310 <400> SEQUENCE: 12
311 ccggaattcg cacataatga cctttca                27
314 <210> SEQ ID NO: 13
315 <211> LENGTH: 26
316 <212> TYPE: DNA
317 <213> ORGANISM: Artificial Sequence
319 <220> FEATURE:
320 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
322 <400> SEQUENCE: 13
323 cgcggatcca tgcctgatgg caattg                26
326 <210> SEQ ID NO: 14
327 <211> LENGTH: 28
328 <212> TYPE: DNA
329 <213> ORGANISM: Artificial Sequence
331 <220> FEATURE:
332 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
334 <400> SEQUENCE: 14
335 ccatcgatga tttcataagc gaaatac                28
338 <210> SEQ ID NO: 15
339 <211> LENGTH: 29
340 <212> TYPE: DNA
341 <213> ORGANISM: Artificial Sequence

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/025,222A

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